T020TT"86225007 Fig. 1

```
   1 CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC
     GGGTGCGCAG GCGTATTTAG TCGTGCGCCG GCCTCTTGGG GCGTTAGAGA CGCGGGTGTT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG

 101 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGAACAACG GGGACAGAAC GCCCCGGCCG CTTCGGGGGC CCGGAAAAGG CACGGCCCAG
     GGTGCCCGGA CTCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTTGC CCCTGTCTTG CGGGGCCGGC GAAGCCCCCG GGCCTTTTCC GTGCCGGGTC
   1                                          M etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly

 201 GACCCAGGGA GGCGCGGGGA GCCAGGCCTG GGCTCCGGGT CCCCAAGACC CTTGTGCTCG TTGTCGCCGC GGTCCTGCTG TTGGTCTCAG CTGAGTCTGC
     CTGGGTCCCT CCGCGCCCCT CGGTCCGGAC CCGAGGCCCA GGGGTTCTGG GAACACGAGC AACAGCGGCG CCAGGACGAC AACCAGAGTC GACTCAGACG
  22   ProArgGl uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSerA laGluSerAla

 301 TCTGATCACC CAACAAGACC TAGCTCCCCA GCAGAGAGCG GCCCCACAAC AAAAGAGGTC CAGCCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC
     AGACTAGTGG GTTGTTCTGG ATCGAGGGGT CGTCTCTCGC CGGGGTGTTG TTTTCTCCAG GTCGGGGAGT CTCCCTAACA CAGGTGGACC TGTGGTATAG
  55  LeuIleThr GlnGlnAspL euAlaProGl nGlnArgAla AlaProGlnG lnLysArgSe rSerProSer GluGlyLeuC ysProProGl yHisHisIle

 401 TCAGAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTGTGATT
     AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CGCGACGTGG TCCACACTAA
 -88 SerGluAspG lyArgAspCy sIleSerCys LysTyrGlyG lnAspTyrSe rThrHisTrp AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer

 501 CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGCGAAG AAGGCACCTT CCGGGAAGAA GATTCTCCTG AGATGTGCCG
     GTCCACTTCA CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTCACACA GTCACGCTTC TTCCGTGGAA GGCCCTTCTT CTAAGAGGAC TCTACACGGC
 122   GlyGluVa lGluLeuSer ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg

 601 GAAGTGCCGC ACAGGGTGTC CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCCTGGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA
     CTTCACGGCG TGTCCCACAG GGTCTCCCTA CCAGTTCCAG CCACTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT
 155  LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerGl yIleIleIle

 701 GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGCTGTGT TTGTTTGCAA GTCTTTACTG TGGAAGAAAG TCCTTCCTTA CCTGAAAGGC ATCTGCTCAG
     CCTCAGTGTC AACGTCGGCA TCAGAACTAA CACCGACACA AACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC
 188 GlyValThrV alAlaAlaVa lValLeuIle ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly IleCysSerGly

 801 GTGGTGGTGG GGACCCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCCTCAA TGAGATCGTG AGTATCTTGC AGCCCACCCA
     CACCACCACC CCTGGGACTC GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT
 222   GlyGlyGl yAspProGlu ArgValAspA rgSerSerGl nArgProGly AlaGluAspA snValLeuAs nGluIleVal SerIleLeuG lnProThrGln

 901 GGTCCCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA
     CCAGGGACTC GTCCTTTACC TTCAGGTCCT CGGTCGTCTC GGTTGTCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT
 255  ValProGlu GlnGluMetG luValGlnGl uProAlaGlu ProThrGlyV alAsnMetLe uSerProGly GluSerGluH isLeuLeuGl uProAlaGlu

1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGCTTCGA TGACTTTGCA GACTTGGTGC
     CGACTTTCCA GAGTCTCCTC CTCCGACGAC CAAGGTCGTT TACTTCCACT AGGGTGACTC TGAGACTCTG TCACGAAGCT ACTGAAACGT CTGAACCACG
 288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG lnCysPheAs pAspPheAla AspLeuValPro
```

```
1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGCG GGCCACAGGG ACACCTTGTA
     GGAAACTGAG GACCCTCGGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTTCC ACCGATTTCG ACTCCGTCGC CCGGTGTCCC TGTGGAACAT
 322   PheAspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluIleLysV alAlaLysAl aGluAlaAla GlyHisArgA spThrLeuTyr

1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCTGCT GGATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG
     GTGCTACGAC TATTTCACCC AGTTGTTTTG GCCCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTGA ACGGTTCGTC
 355  ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln

1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA
     TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTCACAC TAAGAGAAGT CCTTCACTCT
 388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluGl yAsnAlaAsp SerAlaXQQS erOC*

1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC
     GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG

1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT
     GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTCG ACTTACACTA TTATTCCTGT GATACCTTTA

1601 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA TTGTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT
     CAGACCTAGT AAGGCAAACA CGCATGAAAC TCTAAACCAA ACCCTACAGT AACAAAAGTG TCGTGAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA

1701 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAG GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC
     AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTC CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACCGG CGGTACCGG
```

Fig. 1 (cont.)

Fig. 2A

```
  1 MEQRGQNAPAASGARKRHGPGPREARGARPGLRVPKTLVLVVAAVLLLVSAESALITQQD
 61 LAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCLRCTRCD
121 SGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVH
181 KESGIIIGVTVAAVVLIVAVFVCKSLLWKKVLPYLKGICSGGGGDPERVDRSSQRPGAED
241 NVLNEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEAERSQRRRLLVPA
301 NEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAAGHRDTLYTMLIKW
361 VNKTGRDASVHTLLDALETLGERLAKQKIEDHLLSSGKFMYLEGNADSALS
```

Fig. 2B

```
Apo2        EADLVPEDSWEPLMRKLGLMDNEIKVAKAEAA--GHRDTL
DR4         EANIVPEDSWDQLMRQLDLTKNEIDVVRAGTA--GPGDAL
Apo3/DR3    VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR--FRDQQ
TNFR1       VVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR-CLREAQ
Fas/Apo1    IAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKV

Apo2        YTMLIKWVNKTGRD-ASVHTLLDALETLGERLAKQKIED
DR4         YAMLMKWVNKTGRN-ASIHTLLDALERMEERHAKEKIQD
Apo3/DR3    YEMLKRWRQQQP--AGLGAVYAALERMGLDGCVEDLRS
TNFR1       YSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEE
Fas/Apo1    -QLLRNWHQLHGKKEAY-DTLIKDLKKANLCTLAEKIQT
```

Fig. 3

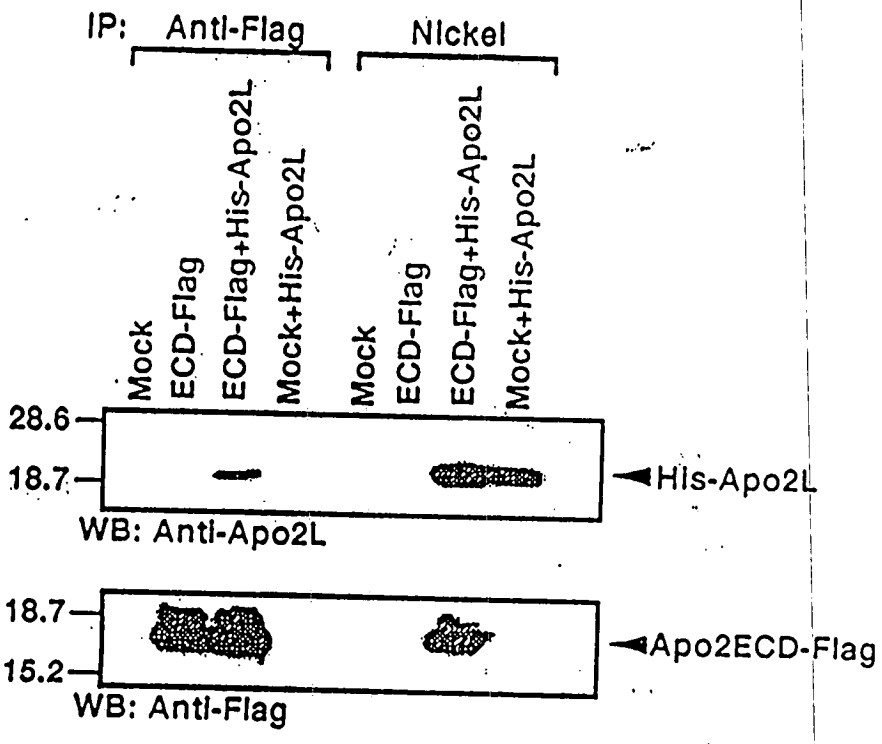
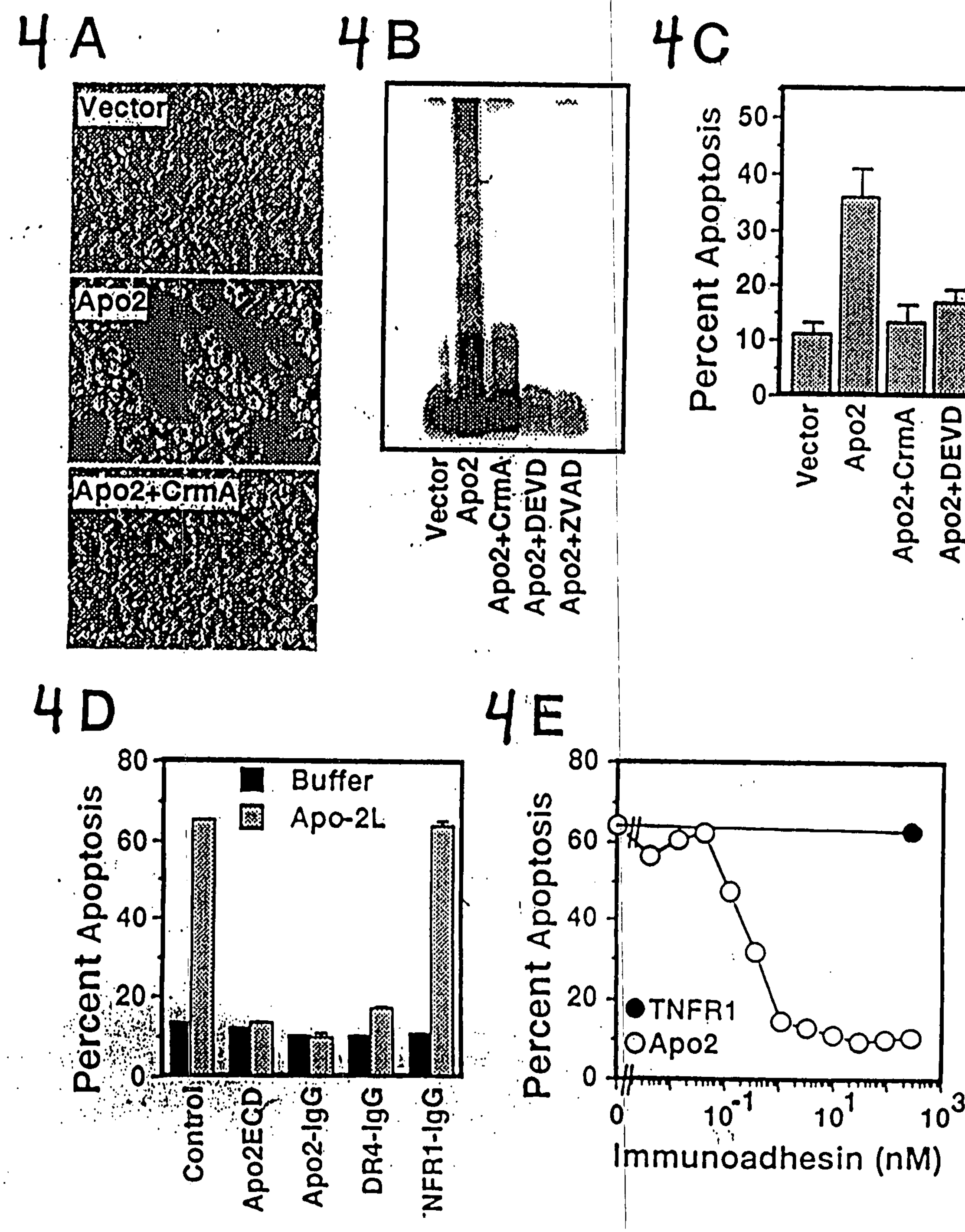
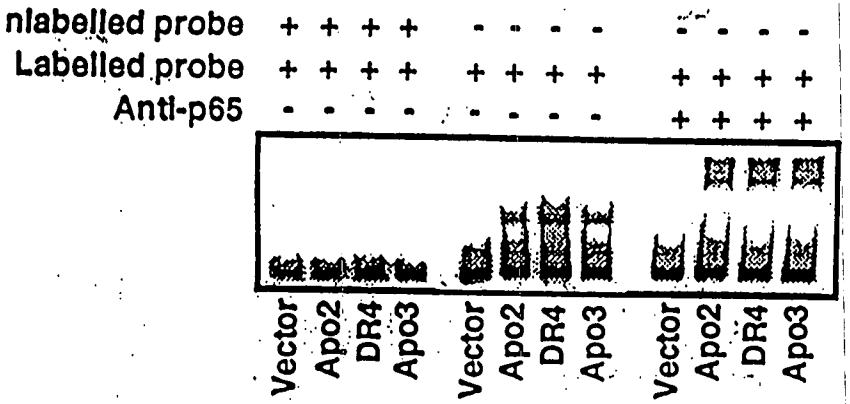

IP: Anti-Flag
Nickel
Mock
ECD-Flag
ECD-Flag+His-Apo2L
Mock+His-Apo2L
Mock
ECD-Flag
ECD-Flag+His-Apo2L
Mock+His-Apo2L
28.6
18.7
His-Apo2L
WB: Anti-Apo2L
18.7
15.2
Apo2ECD-Flag
WB: Anti-Flag

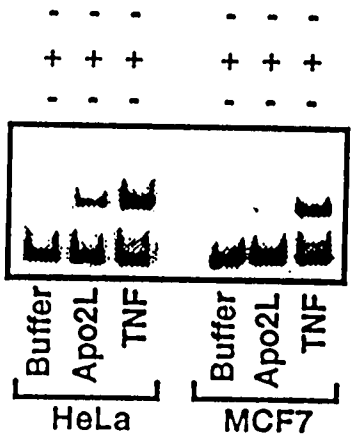
Fig. 4



A



5B



5C

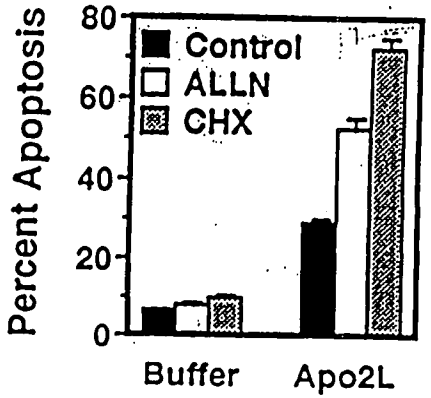


FIG. 5

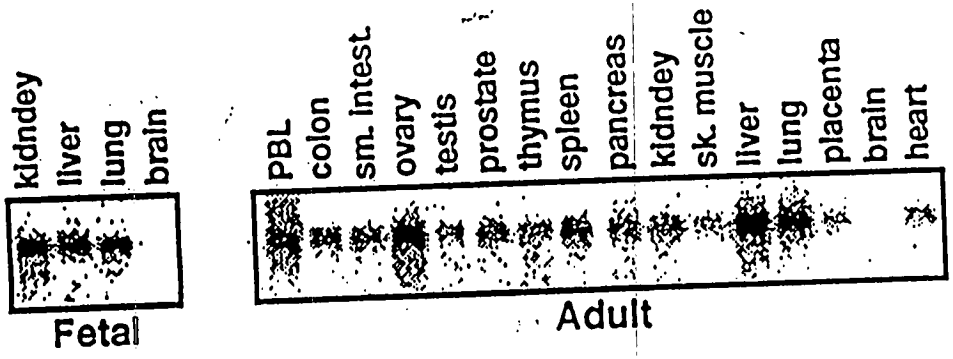


FIG. 6A

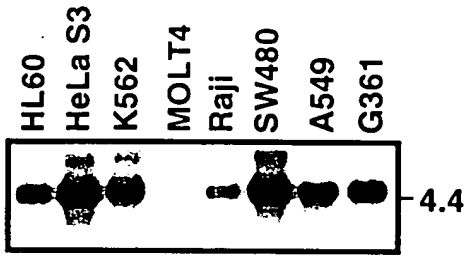


Fig. 6B

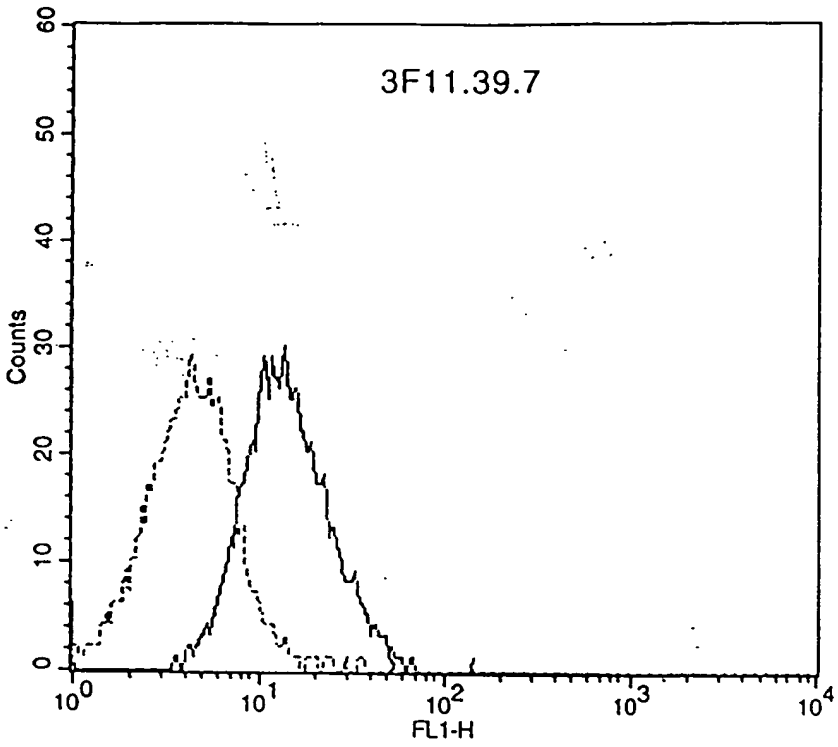


Fig. 7

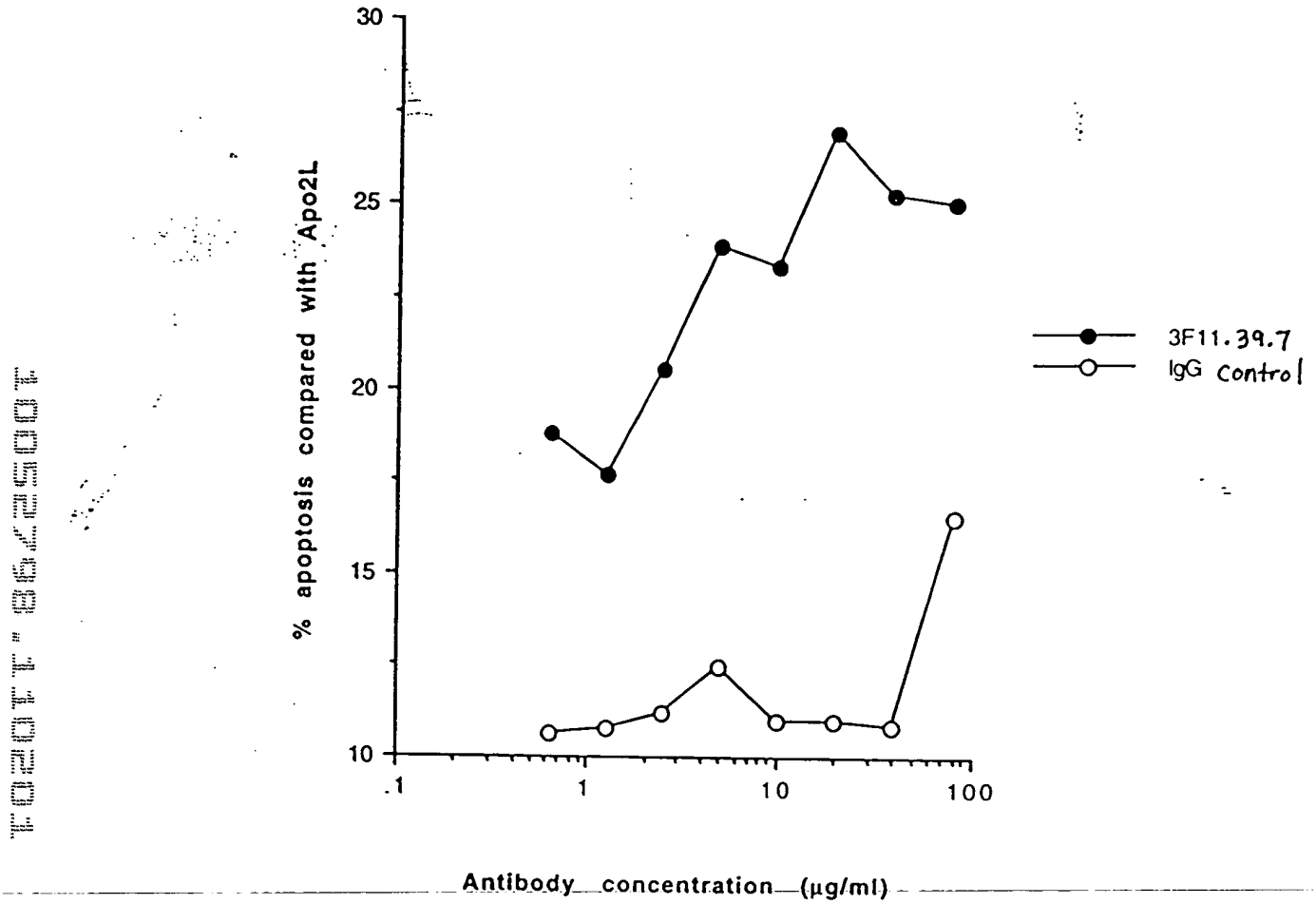

30
25
20
15
10
.1
1
10
100
% apoptosis compared with Apo2L
Antibody concentration (µg/ml)
3F11.39.7
IgG control

Fig. 8

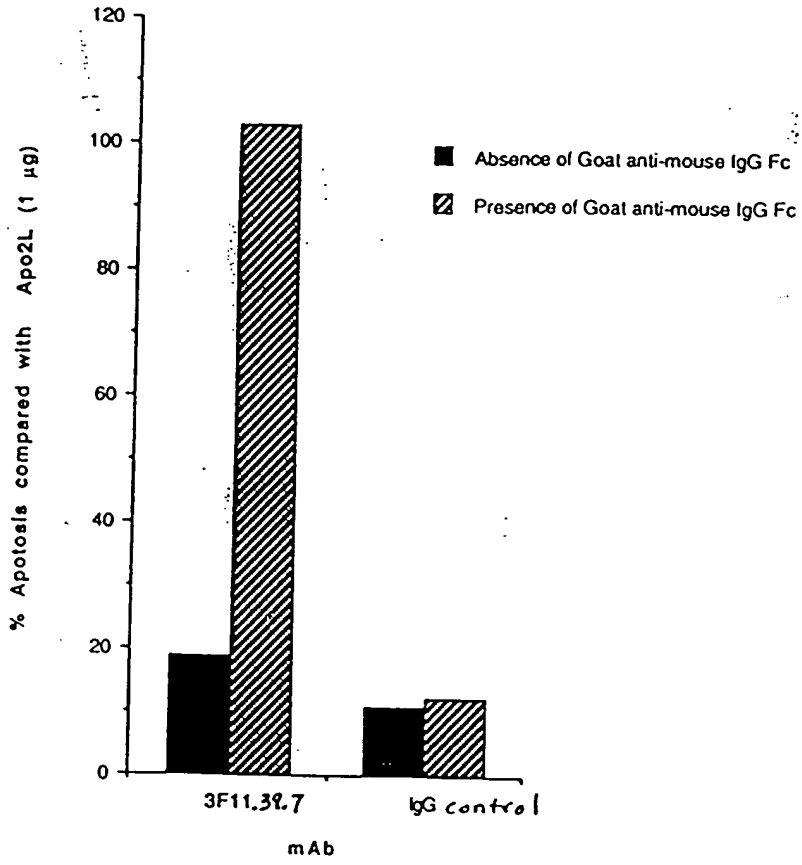


Fig. 9

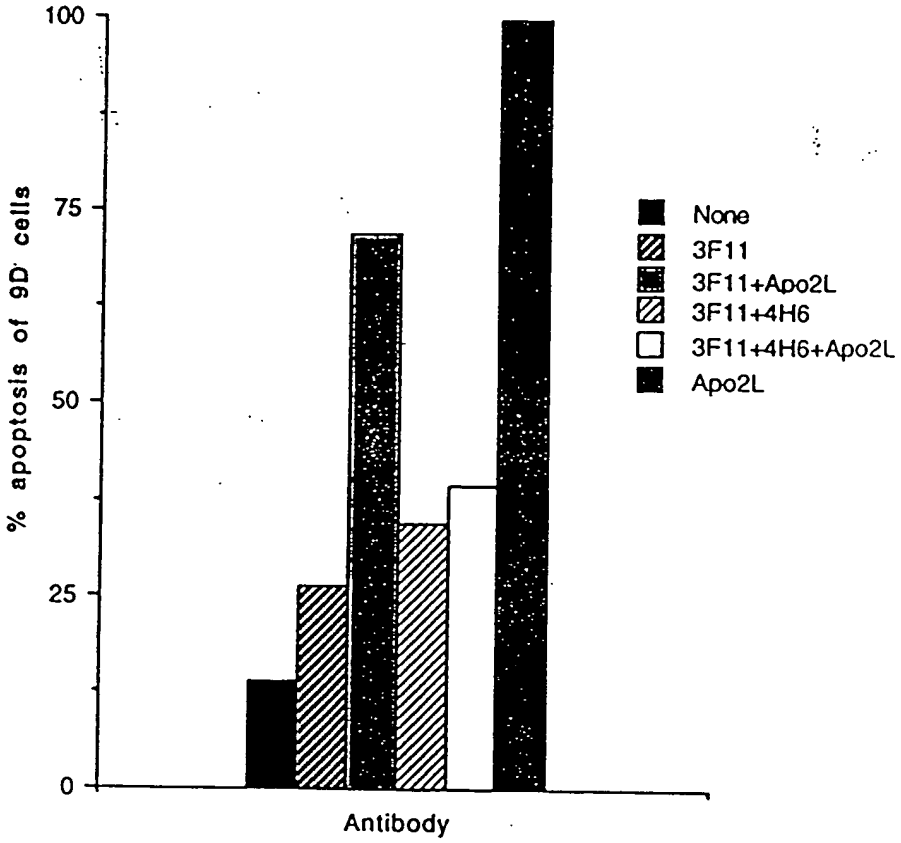

100
75
50
25
0
% apoptosis of 9D cells
Antibody
None
3F11
3F11+Apo2L
3F11+4H6
3F11+4H6+Apo2L
Apo2L

Fig : 10

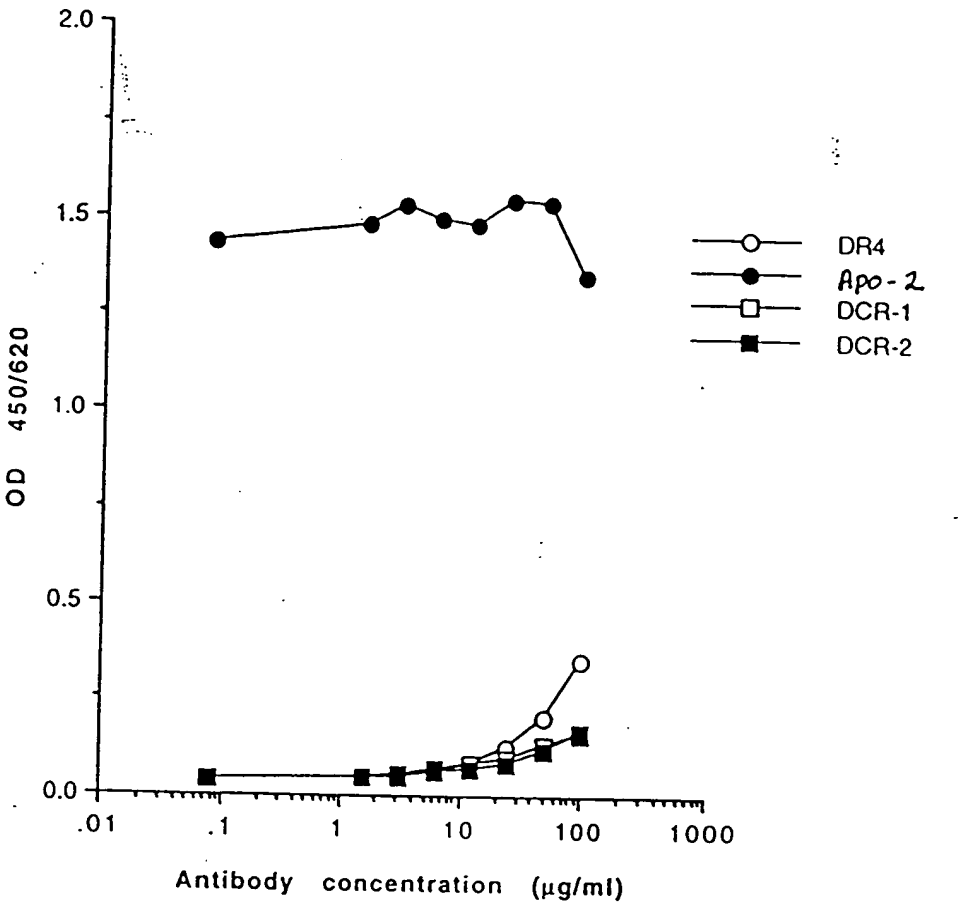

2.0
1.5
1.0
0.5
0.0
OD 450/620
.01
.1
1
10
100
1000
Antibody concentration (µg/ml)
DR4
Apo-2
DCR-1
DCR-2

Fig. 11

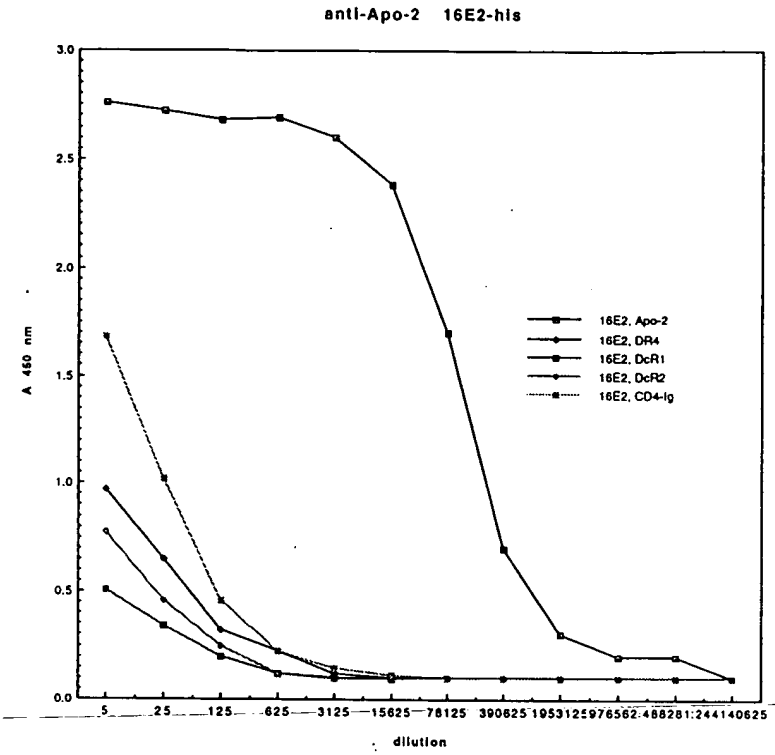


Fig. 12A

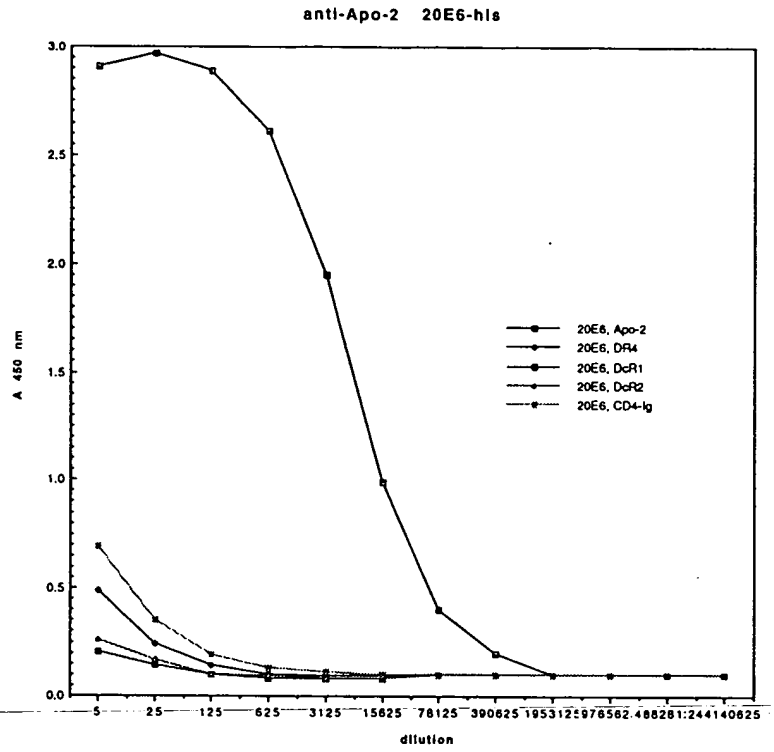

anti-Apo-2 20E6-his
A 450 nm
3.0
2.5
2.0
1.5
1.0
0.5
0.0
20E6, Apo-2
20E6, DR4
20E6, DcR1
20E6, DcR2
20E6, CD4-Ig
5
25
125
625
3125
15625
78125
390625
1953125
9765625
48828125
244140625
dilution

Fig. 12B

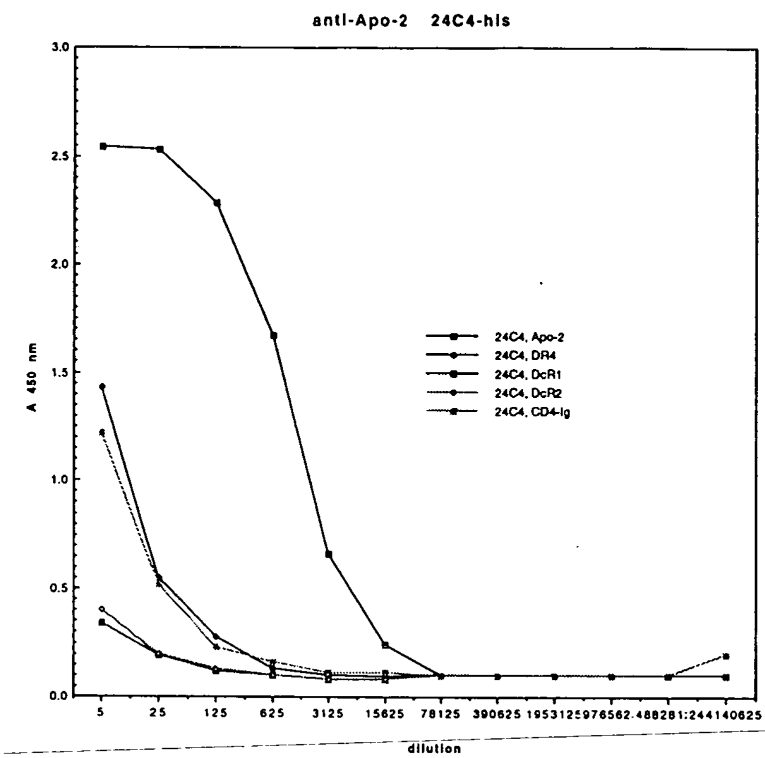
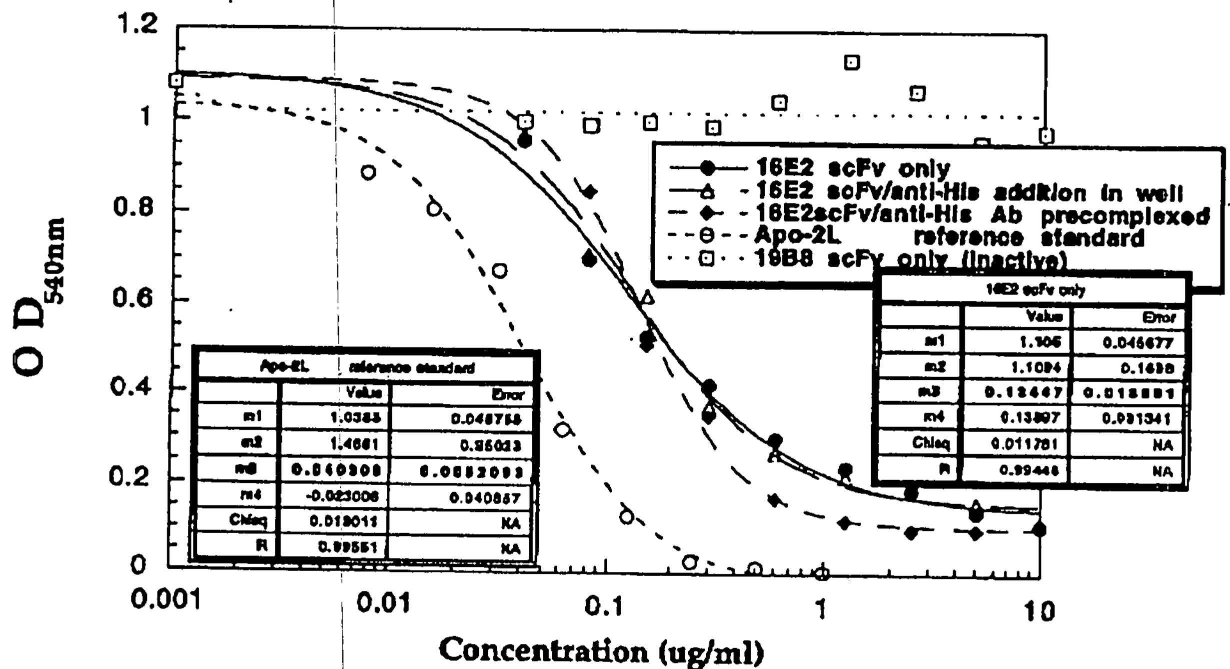


Fig. 12C



1.2
1
0.8
0.6
0.4
0.2
0
O D540nm
0.001
0.01
0.1
1
10
Concentration (ug/ml)
16E2 scFv only
16E2 scFv/anti-His addition in well
16E2scFv/anti-His Ab precomplexed
Apo-2L reference standard
19B8 scFv only (inactive)
Apo-2L reference standard
Value Error
m1 1.0385 0.048755
m2 1.4661 0.25023
m3 0.040308 0.0052093
m4 -0.023006 0.040857
Chisq 0.019011 NA
R 0.99551 NA
16E2 scFv only
Value Error
m1 1.106 0.045677
m2 1.1094 0.1638
m3 0.12447 0.015881
m4 0.13897 0.031341
Chisq 0.011781 NA
R 0.99446 NA

Fig. 13A

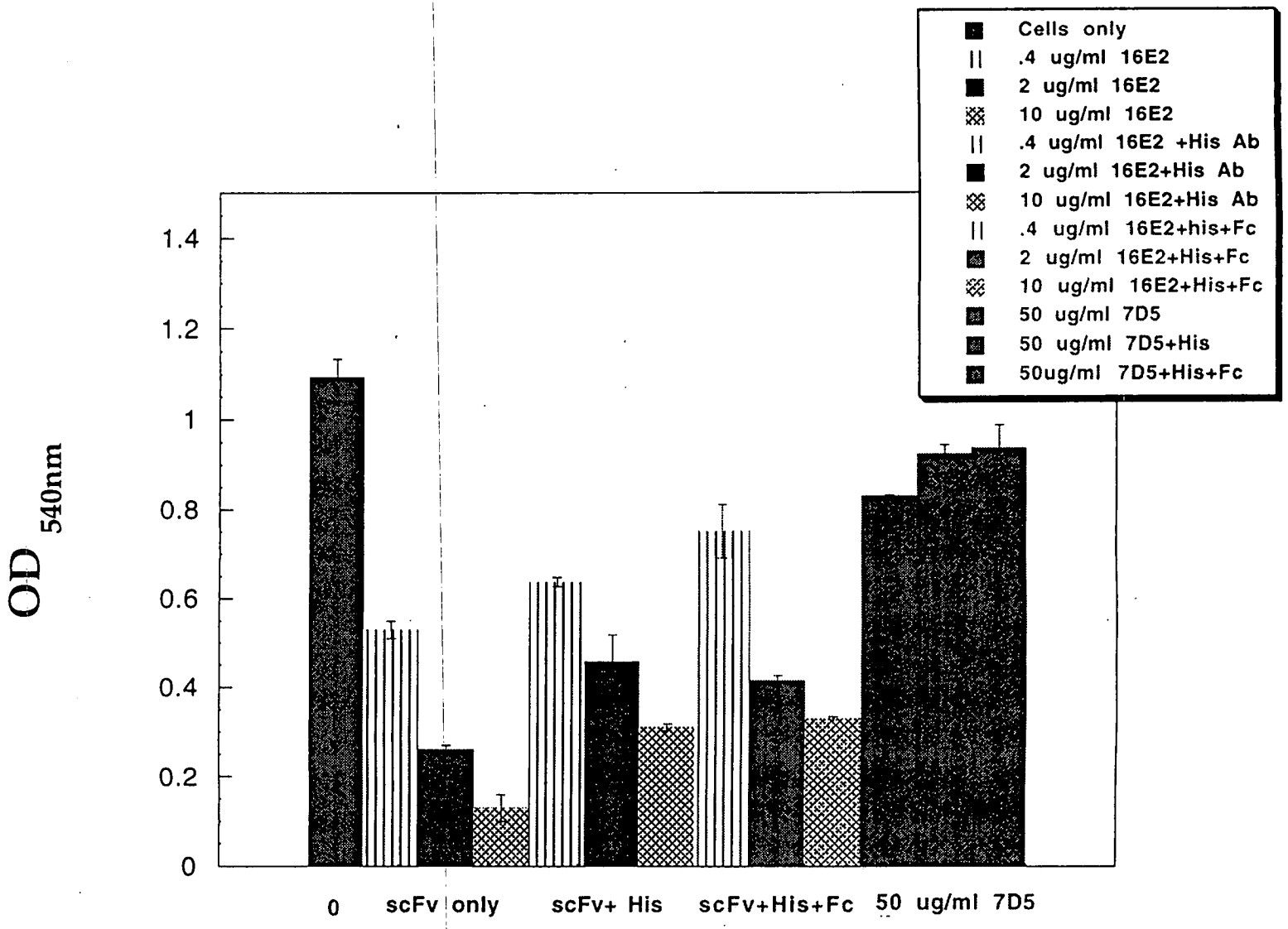


Fig. 13B

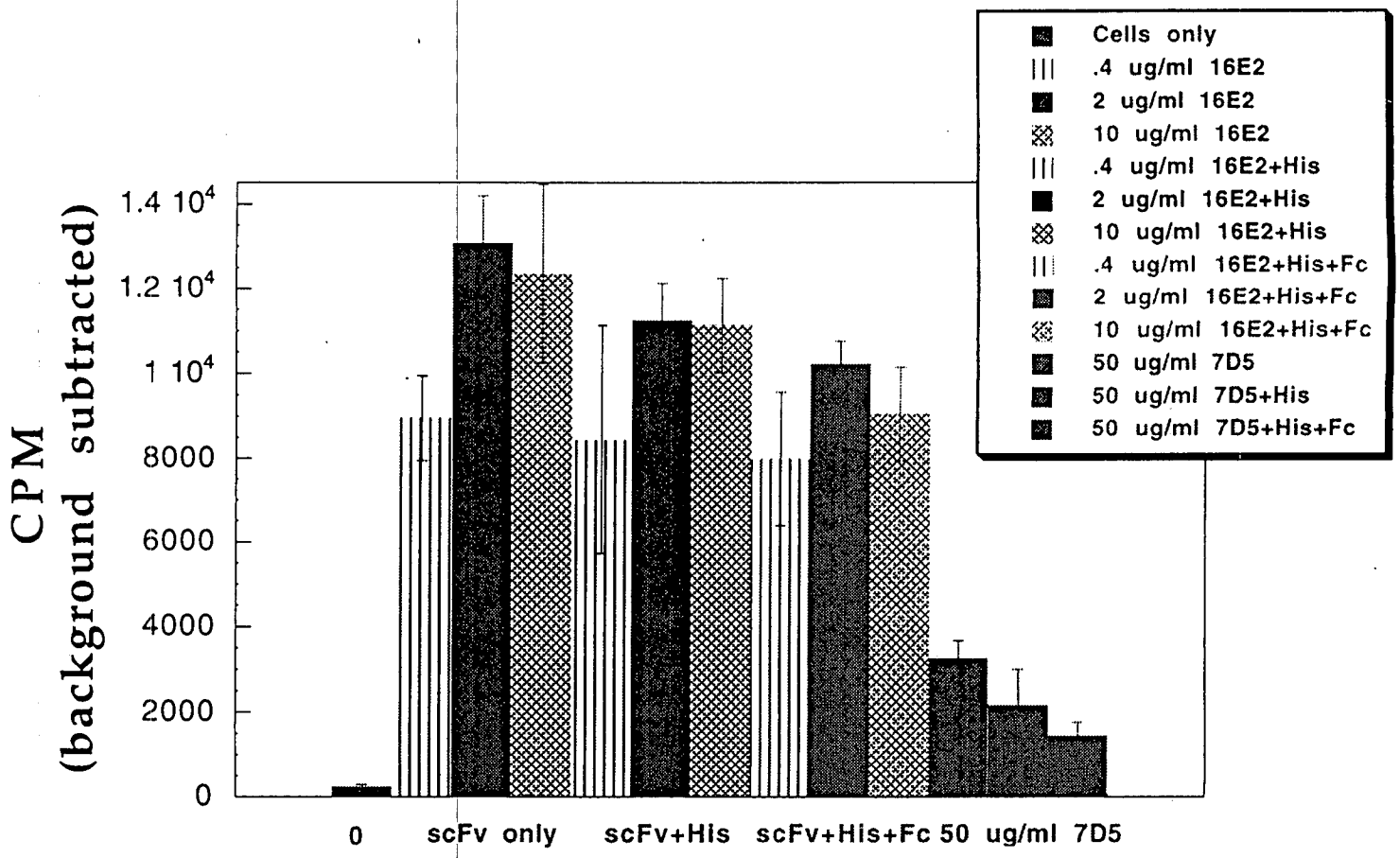
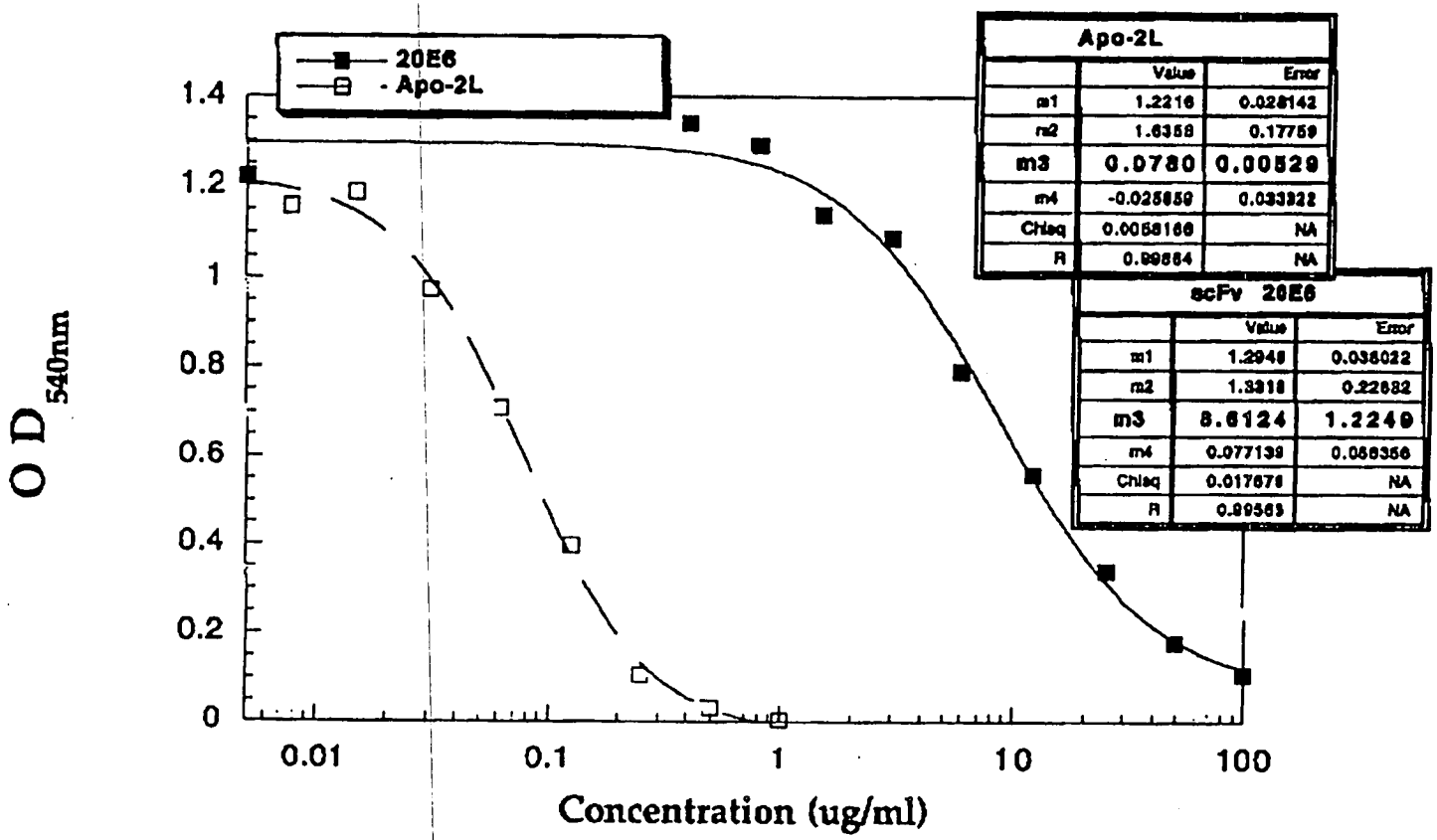


Fig. 13C



Apo-2L		
	Value	Error
m1	1.2216	0.028142
m2	1.6358	0.17759
m3	0.0780	0.00529
m4	-0.025859	0.033922
Chisq	0.0058166	NA
R	0.99564	NA

scFv 20E6		
	Value	Error
m1	1.2948	0.038022
m2	1.3318	0.22682
m3	8.6124	1.2249
m4	0.077139	0.056356
Chisq	0.017676	NA
R	0.99563	NA

Fig 14A

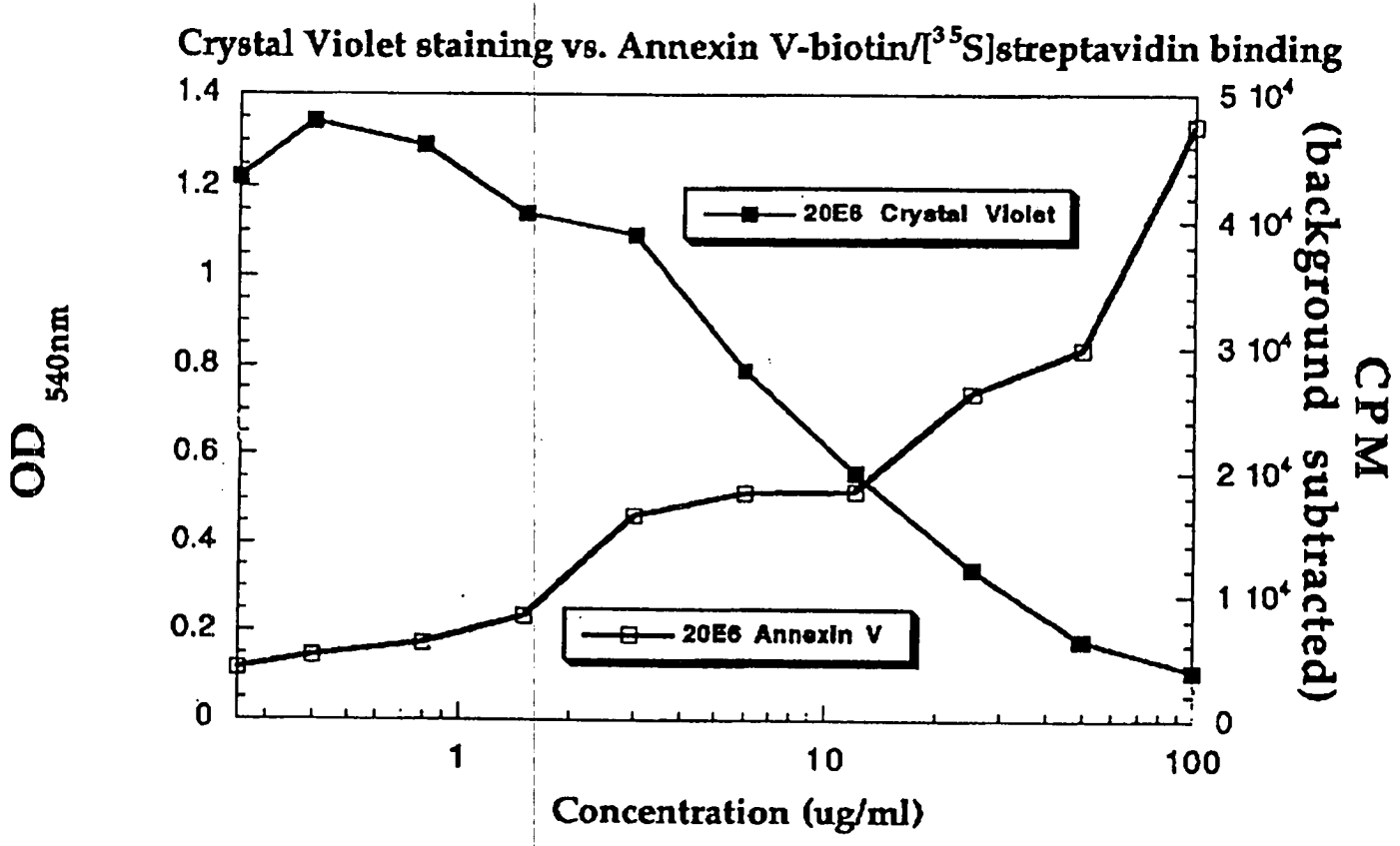
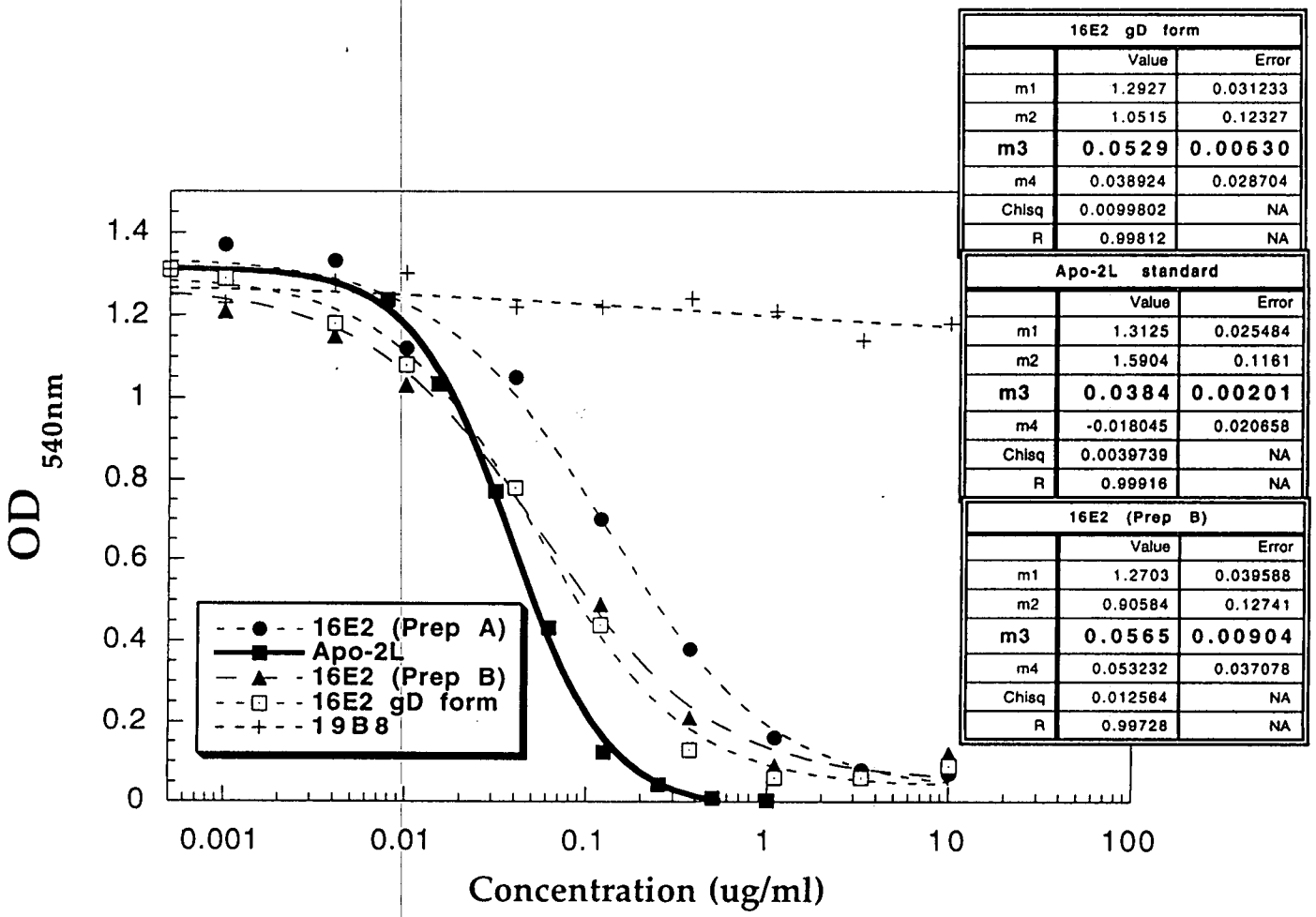


Fig. 14B



16E2 gD form		
	Value	Error
m1	1.2927	0.031233
m2	1.0515	0.12327
m3	**0.0529**	**0.00630**
m4	0.038924	0.028704
Chisq	0.0099802	NA
R	0.99812	NA

Apo-2L standard		
	Value	Error
m1	1.3125	0.025484
m2	1.5904	0.1161
m3	**0.0384**	**0.00201**
m4	-0.018045	0.020658
Chisq	0.0039739	NA
R	0.99916	NA

16E2 (Prep B)		
	Value	Error
m1	1.2703	0.039588
m2	0.90584	0.12741
m3	**0.0565**	**0.00904**
m4	0.053232	0.037078
Chisq	0.012564	NA
R	0.99728	NA

Fig. 14C

ATGACCATGA TTACGCCAAG CTTTGGAGCC TTTTTTTTGG AGATTTTCAA 50

CGTGAAAAAA TTATTATTCG CAATTCCTTT AGTTGTTCCT TTCTATGCGG 100

CCCAGCCGGC CATGGCCGAG GTGCAGCTGG TGCAGTCTGG GGGAGGTGTG 150

GAACGGCCGG GGGGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGATTCAC 200

CTTTGATGAT TATGGCATGA GCTGGGTCCG CCAAGCTCCA GGGAAGGGGC 250

TGGAGTGGGT CTCTGGTATT AATTGGAATG GTGGTAGCAC AGGATATGCA 300

GACTCTGTGA AGGGCCGAGT CACCATCTCC AGAGACAACG CCAAGAACTC 350

CCTGTATCTG CAAATGAACA GCCTGAGAGC CGAGGACACG GCCGTATATT 400

ACTGTGCGAA AATCCTGGGT GCCGGACGGG GCTGGTACTT CGATCTCTGG 450

GGGAAGGGGA CCACGGTCAC CGTCTCGAGT GGTGGAGGCG GTTCAGGCGG 500

AGGTGGCAGC GGCGGTGGCG GATCGTCTGA GCTGACTCAG GACCCTGCTG 550

TGTCTGTGGC CTTGGGACAG ACAGTCAGGA TCACATGCCA AGGAGACAGC 600

CTCAGAAGCT ATTATGCAAG CTGGTACCAG CAGAAGCCAG GACAGGCCCC 650

TGTACTTGTC ATCTATGGTA AAAACAACCG GCCCTCAGGG ATCCCAGACC 700

GATTCTCTGG CTCCAGCTCA GGAAACACAG CTTCCTTGAC CATCACTGGG 750

GCTCAGGCGG AAGATGAGGC TGACTATTAC TGTAACTCCC GGGACAGCAG 800

TGGTAACCAT GTGGTATTCG GCGGAGGGAC CAAGCTGACC GTCCTAGGTG 850

CGGCCGCACA TCATCATCAC CATCACGGGG CCGCAGAACA AAAACTCATC 900

TCAGAAGAGG ATCTGAATGG GGCCGCATAG 930

Fig. 15A

ATGACCATGA TTACGCCAAG CTTTGGAGCC TTTTTTTTGG AGATTTTCAA 50

CGTGAAAAAA TTATTATTCG CAATTCCTTT AGTTGTTCCT TTCTATGCGG 100

CCCAGCCGGC CATGGCCGGG GTGCAGCTGG TGGAGTCTGG GGGAGGCTTG 150

GTCCAGCCTG GGGGGTCCCT GAGACTCTCC TGTGCAGCCT CTGGATTCAC 200

CTTTAGTAGC TATTGGATGA GCTGGGTCCG CCAGGCTCCA GGGAAGGGGC 250

TGGAGTGGGT GGCCAACATA AAGCAAGATG GAAGTGAGAA ATACTATGTG 300

GACTCTGTGA AGGGCCGATT CACCATCTCC AGAGACAACG CCAAGAACTC 350

ACTGTATCTG CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT 400

ACTGTGCGAG AGATCTTTTA AAGGTCAAGG GCAGCTCGTC TGGGTGGTTC 450

GACCCCTGGG GGAGAGGGAC CACGGTCACC GTCTCGAGTG GTGGAGGCGG 500

TTCAGGCGGA GGTGGTAGCG GCGGTGGCGG ATCGTCTGAG CTGACTCAGG 550

ACCCTGCTGT GTCTGTGGCC TTGGGACAGA CAGTCAGGAT CACATGCCAA 600

GGAGACAGCC TCAGAAGCTA TTATGCAAGC TGGTACCAGC AGAAGCCAGG 650

ACAGGCCCCT GTACTTGTCA TCTATGGTAA AAACAACCGG CCCTCAGGGA 700

TCCCAGACCG ATTCTCTGGC TCCAGCTCAG GAAACACAGC TTCCTTGACC 750

ATCACTGGGG CTCAGGCGGA AGATGAGGCT GACTATTACT GTAACTCCCG 800

GGACAGCAGT GGTAACCATG TGGTATTCGG CGGAGGGACC AAGCTGACCG 850

TCCTAGGTGC GGCCGCACAT CATCATCACC ATCACGGGGC CGCAGAACAA 900

AAACTCATCT CAGAAGAGGA TCTGAATGGG GCCGCATAG 939

Fig. 15B

ATGACCATGA TTACGCCAAG CTTTGGAGCC TTTTTTTTGG AGATTTTCAA 50

CGTGAAAAAA TTATTATTCG CAATTCCTTT AGTTGTTCCT TTCTATGCGG 100

CCCAGCCGGC CATGGCCCAG GTGCAGCTGG TGCAGTCTGG GGGAGGCGTG 150

GTCCAGCCTG GGCGGTCCCT GAGACTCTCC TGTGCAGCTT CTGGGTTCAT 200

TTTCAGTAGT TATGGGATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC 250

TGGAGTGGGT GGCAGGTATT TTTTATGATG GAGGTAATAA ATACTATGCA 300

GACTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC 350

GCTGTATCTG CAAATGAACA GCCTGAGAGC TGAGGACACG GCTGTGTATT 400

ACTGTGCGAG AGATAGGGGC TACTACTACA TGGACGTCTG GGGCAAAGGG 450

ACCACGGTCA CCGTCTCCTC AGGTGGAGGC GGTTCAGGCG GAGGTGGCTC 500

TGGCGGTGGC GGATCGCAGT CTGTGTTGAC GCAGCCGCCC TCAGTGTCTG 550

GGGCCCCAGG ACAGAGGGTC ACCATCTCCT GCACTGGGAG AAGCTCCAAC 600

ATCGGGGCAG GTCATGATGT ACACTGGTAC CAGCAACTTC CAGGAACAGC 650

CCCCAAACTC CTCATCTATG ATGACAGCAA TCGGCCCTCA GGGGTCCCTG 700

ACCGATTCTC TGGCTCCAGG TCTGGCACCT CAGCCTCCCT GGCCATCACT 750

GGGCTCCAGG CTGAAGATGA GGCTGATTAT TACTGCCAGT CCTATGACAG 800

CAGCCTGAGG GGTTCGGTAT TCGGCGGAGG GACCAAGGTC ACTGTCCTAG 850

GTGCGGCCGC ACATCATCAT CACCATCACG GGGCCGCAGA ACAAAAACTC 900

ATCTCAGAAG AGGATCTGAA TGGGGCCGCA TAG 933

Fig. 15C

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                          signal                                          Heavy chain
Apo-2.16E2.his        1   MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAEVQLVQSGGGV
Apo-2.20E6.his        1   MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGL
Apo-2.24C4.his        1   MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAQVQLVQSGGGV

                                             CDR1                    CDR2
Apo-2.16E2.his       51   ERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGYA
Apo-2.20E6.his       51   VQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV
Apo-2.24C4.his       51   VQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYA

                                                                   CDR3
Apo-2.16E2.his      101   DSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKIL----GAGRGWY
Apo-2.20E6.his      101   DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGW-
Apo-2.24C4.his      101   DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD--------RGYY

                                                             Light chain
Apo-2.16E2.his      147   F-DLWGKGTTVTVSSGGGGSGGGGSGGGGS-SELTQDPAVSVALGQTVRI
Apo-2.20E6.his      150   F-DPWGRGTTVTVSSGGGGSGGGGSGGGGS-SELTQDPAVSVALGQTVRI
Apo-2.24C4.his      143   YMDVWGKGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTI

                            CDR1                       CDR2
Apo-2.16E2.his      195   TCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSG
Apo-2.20E6.his      198   TCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSG
Apo-2.24C4.his      193   SCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSRSG

                                                 CDR3
Apo-2.16E2.his      242   NTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHH
Apo-2.20E6.his      245   NTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHH
Apo-2.24C4.his      243   TSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHH

Apo-2.16E2.his      292   HGAAEQKLISEEDLNGAA
Apo-2.20E6.his      295   HGAAEQKLISEEDLNGAA
Apo-2.24C4.his      293   HGAAEQKLISEEDLNGAA
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Fig. 16